

Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	0.52	0.50	0	1
Marital status	0.65	0.48	0	1
Education	12.8	2.1	9	16
Income	15.2	8.5	5	35
Occupation	1.2	0.8	0	2
Health status	0.75	0.42	0	1
Stress level	2.1	1.5	1	5
Life satisfaction	3.8	1.2	1	5
Depression	0.35	0.48	0	1
Loneliness	0.65	0.45	0	1
Self-esteem	2.5	1.0	1	4
Resilience	3.2	1.1	1	5
Optimism	3.5	1.0	1	5
Gratitude	3.0	1.2	1	5
Forgiveness	3.3	1.1	1	5
Empathy	3.1	1.0	1	5
Prosocial behavior	3.4	1.1	1	5
Altruism	3.2	1.0	1	5
Compassion	3.3	1.1	1	5
Kindness	3.4	1.0	1	5
Generosity	3.5	1.1	1	5
Helpfulness	3.6	1.0	1	5
Cooperativeness	3.7	1.1	1	5
Teamwork	3.8	1.0	1	5
Leadership	3.9	1.1	1	5
Communication	4.0	1.0	1	5
Conflict resolution	4.1	1.1	1	5
Problem solving	4.2	1.0	1	5
Decision making	4.3	1.1	1	5
Goal setting	4.4	1.0	1	5
Time management	4.5	1.1	1	5
Organization	4.6	1.0	1	5
Productivity	4.7	1.1	1	5
Efficiency	4.8	1.0	1	5
Quality of work	4.9	1.1	1	5
Job satisfaction	5.0	1.0	1	5
Work-life balance	5.1	1.1	1	5
Overall well-being	5.2	1.0	1	5

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h: 1 MSGSTQPVAAQTWRATPPHSLSYPVQIARTHTDVGLEYQHHSRDYASHLSPGSIQPPRRRPSLLSEFQPGNERSQELHLRPESHSLPELGKXSM
m: 1 -----A-----GI-----S-----P-----T-----S-----RTF-----PDI

h: 101 EFIESKRPRLELLPDPLLRLPSPLLATGQPAGSEDLTKDRSLTGKLEPVSPSPPHTDPELELVPPRLSKEELIQN.MDRVDREITMVEQQISKLKKKQQQ
m: 101 --T-----T-----S-----A-----A-----A-S-----RL-----

h: 200 LEEEAAPPEPEKPVSPPIESKHSRLVQIIYDENRKKAAEAHRILEGLGPQVELPLYNQPSDTROYHENIKINQAMRKKLILYFKRRNHARKQWEQKFC
m: 201 -----R-----

h: 300 QRYDQLMEAWKVERIENNPRRRAKESKVREYYEQFPPIRKKQRELQERMQ.RVGQRGSGLSMSPARSEHEVSEIIDGLSEQENLEKQMRQLAVIPMML
m: 301 -----S-----A-----RHVV-----

h: 399 YDADQQRIRKFINMNGLMADPMKVYKDRQVMNMWSEQEKETFREKFMQHPKNFGLIASFLERKTVACVLYYYLTCKKNENYKSLVRRSYRRRGKSQQQQQQ
m: 401 .RR-----D-----T-----RD-----

h: 499 QQQQQQQQQQMPRSSQEEKDEKEKEKEAEKEEKEPEVENDKEDLLKEKTDSTGEDNDEKEAVASKRKTANSQGRRKGRITRSMANEANSEEAITPQ
m: 500 -----A-----E-----D-----QDA--E--E-S-----H--TA--

h: 599 QSaelasmelnessrwteeemetakkgllEHGRNWSAIARMVGSKTVSQCKNFYFNYKKRQNLDEILQHQHKLKMEKERNARRKKKKAPAAASEEAFFPV
m: 596 --S-----M-----T-----T-----A
m: AC: --S-----M-----HQTPGPGARLLTQQELRAPIPSTPQLQPHSHRPHPSKEPCTPPCQSGPAGAHGLRSAPRKDSK*

h: 699 VEDEEMEASGVTGNEEEMVEEAET.....VNSSDTEsIPSPHTEAAKDTGQNGPKPPATLGADGPPPGPPTPPPEDIPAPTESTP
m: 696 A-----SA-----LA-----SQASGNEVPRVGECSGPA-----V--RS--T-----G-EALPAATQP-VP--E-PAA--A-PS-

h: 781 ASEATLAPTPPPAPPFPSSPPVPKKEEKEETAAAPPVEEGEEQKPPAAEELAVDTGKAEPP.....VKSECTEEAEEGPA.KGKDAAEAEEATAE
m: 793 VPD-SGPPS-E-S-S.-AA--AT-D-D-Q-APA-P--QT-DAK--SEAE...I-V--P--EASEEPPES--DHK--T--E-ED-A-GT--I-TVS-

h: 871 RALKAekEGGSGRATTAKSSGAPQDSSSATCSADEVDEAEGGDKNRLLSPRPSLLTPTGDPRANASPKPLDLKQLKQRAAIIPIQVTKVHEPPRED
m: 889 AP--V-.EAGSKAAV-KGS--T-----P-----G-----A-----ST-----

MEAWDAH-P->(SMRT)

h: 971 AAPTkpAPPAPPPPPQNLQPESDAPQPGSSPRGKSRSAPPADKEAKPVFFPAFAAEBAQKLPGDPPCWTSGLFFVPVPPREVIKASPHAPDPsAFsYAPP
m: 987 TV-P-V-V--T-H--G-VS--S-G-----V--E--A-----PT-G-SYRLS-HA.GHR--.SH-----T-TR--.L--T--

h: 1071 GHPLPLGLHDTARPVLP RPPTISNPPPLISSAKHPSVLERQIGAISQGMsvQLHVPYSEHAKAPVGPVMTMGLPLPMDPKKLAPFSGVKQEQLSPRGQAGP
m: 1083 -----S-----G-----R--H-----M--L--E--AV-----GTALAPPVEA--ASQ..

h: 1171 PESLGVPTAQEASVLRGTALGsvPGGSITKGIpSTRVPDSAITYRGSIthGTPADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIEGKKGHVLSY
m: 1179 .....Y-GC-R-QLQRLYH....PR-----S--V-----A--T-----

h: 1271 EGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGLMGRAIPPERHSPHHLKEQHHRGSITQGIpRSYVEAQEDYLREAKLLKR
m: 1243 -----S-----TVT-----Q-----

h: 1371 EGTppppPPSRDLTEAYKTQ...ALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHDVRSLI
m: 1341 -----P-----T--PRPLDP-----T--V-----R-----S--PS--T-----

h: 1468 GSPGRtFPpVHPLDVMADARALERACyEESLKSrPGTASSSGGSiARGAPViVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLSSS
m: 1441 -----P--AL-----I-----S--S-GA--T--V-----TS-----T-----L--

h: 1568 KASQDRKLtSTPREIAKSPHSTVPEHHPHPIsPYEHLRgSVGDLYRSHIPLAFDPTsIPRGiPLD.AAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDT
m: 1541 -----T-----G-----EA-----S-----

M->(TRAC1)

h: 1667 AALENRQTIINDYITSQqMHNTATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPTAPQPFSSRHSSSP
m: 1641 -----A-S-----S-----I-----P--H--

h: 1767 LSPGGPthLTkPTTTSSSERERDRDRERDREREKSILtSTTTVEHAPIWRPGTEQSSGSSGSSGGGGSSSRPASHSHAHQHSPIsPRTQDALQQRPS
m: 1741 -----A--A-----E-E-----G-----

h: 1867 VLHNTGMKGIIITAVEPSKPTVLRSTSTSSPVRPAATFPpATHCPLGGTLdGVYPTLMEPVLLPKEApRVARPERPRADTGHaFLAKPPARSGLepASSPS
m: 1825 -----S--VV-S--GT-----E-----TS-----V-G--T-----

h: 1967 KGSEPRPLVPPVSGHATIARTPAKNLAPHHASPDPPAPPASADPHREKTQSKPFSIQELELRSLGyH.GSSYSPEGVEPVSPVSSPSLTHDKGLPKHLE
m: 1922 -S---S-A--S-S-TA-----S-----G.-T--L-----S-AG--D--I-----S-P--

h: 2066 ELDKSHLEGLERLPKQPGPVKLGEAAHLPHLRPLPESQPSsPLLQTAPGVKGHQrVVTLAQHISEViTQDYTRHHPQQLSAPLPAPLYSFPFGASCPVLD
m: 2021 --E-----H-----M--SA-----I-----G-----

h: 2166 LRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGIEpVSPPEGMTEPGHSRSaVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKL
m: 2121 -----T-----S-----SS--A-----A-----G-----

h: 2266 TESNSAMVSKKQEIINKLNTHNrNEPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEESpPLSANAFNPLNASa
m: 2220 -----G-----A--C-----P--G-----

h: 2366 SLP.AAMPITAADGRSDHTLTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDcNRRTPLTNrVWEDRPSSAGSTFPpYNPLIMRLQAG
m: 2320 --A-----T-----A-----

h: 2465 VMASPPPPGLPAGSGPLAGPHAWDEEPKPLLCsQYETLSDSE 2507
m: 2420 -----A-----2462

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Fig. 2

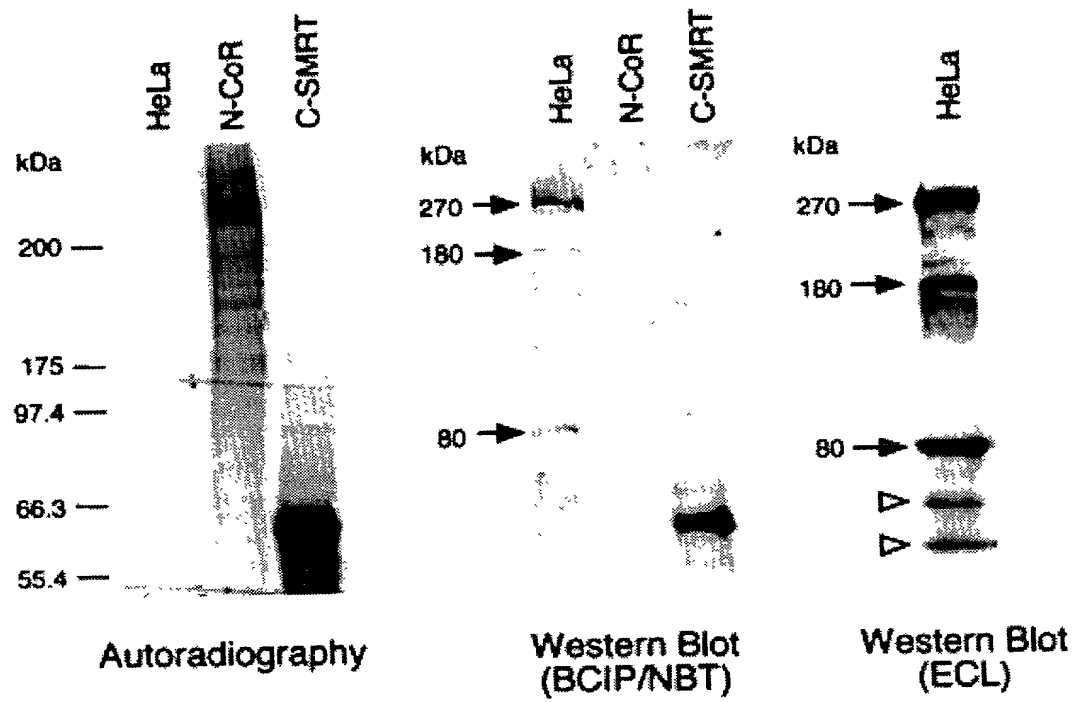


Fig. 3

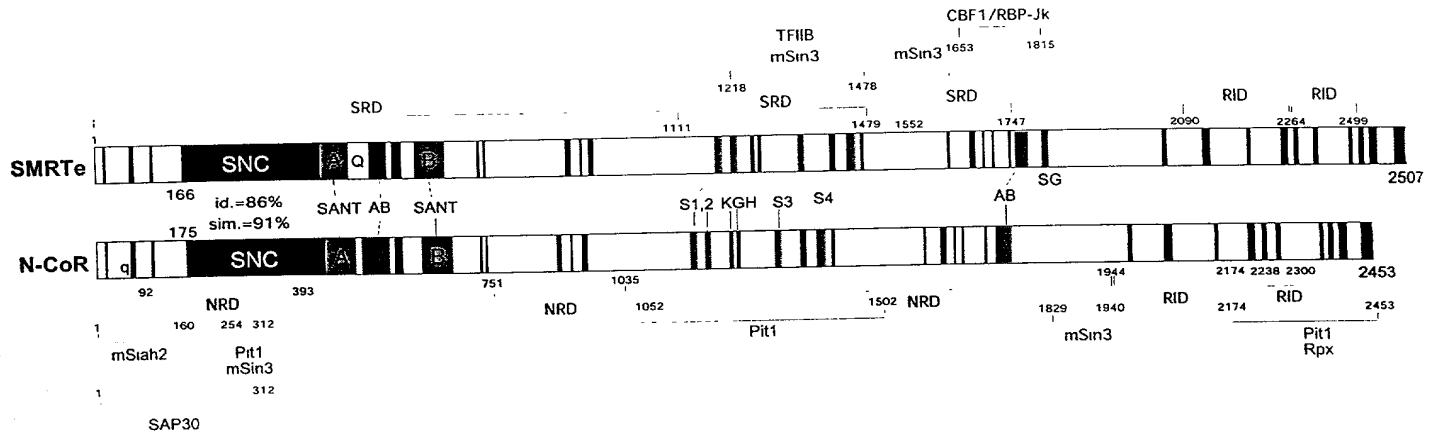


Fig. 4

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mN 175 RLSKEELIQS.MDRVDREITAKVEQQILKLKKKQQQLEEEAAKPPEPEKPV

hS 215 SPPPIESKHRSIVQIIYDENRKKAEAAHRILEGLGPQVELPLYNQPSDTR
mS 216 SPPPIESKHRSIVQIIYDENRKKAEAAHRILEGLGPQVELPLYNQPSDTR
hN 224 SPPPIVEQKHRSIVQIIYDENRKKAEAAHRIEGLGPKVELPLYNQPSDTK
mN 224 SPPPIVEQKHRSIVQIIYDENRKKAEAAHRIEGLGPKVELPLYNQPSDTK

hS 265 QYHENIKINQAMRKKLILYFKRRNHARKQWEQKFCORYDQLEAWKEKKVE
mS 266 QYHENIKINQAMRKKLILYFKRRNHARKQWEQKFCORYDQLEAWKEKKVE
hN 274 VYHENIKINQVMRKKLILYFKRRNHARKQWEQKFCORYDQLEAWKEKKVD
mN 274 VYHENIKINQVMRKKLILYFKRRNHARKQWEQKFCORYDQLEAWKEKKVD

hS 315 RIENNPRRRAKESKVREYYEKQFPEIRKQRELOQERMO.RVGQRGSGLSMS
mS 316 RIENNPRRRAKESKVREYYEKQFPEIRKQRELOQERMOSRVGQRGSGLSMS
hN 324 RIENNPRRRAKESKVREYYEKQFPEIRKQRELOQERFO.RVGQRGAGLSAT
mN 324 RIENNPRRRAKESKVREYYEKQFPEIRKQRELOQERFO.RVGQRGAGLSAT

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mS 366 AARSEHEVSEIIDGLSEQENLEKQMRQLAVIRHVV.RRDOORIKFINMNG
hN 373 IARSEHEVSEIIDGLSEQENNEKQMRQLSVIPPMIFDAEQRRVKFINMNG
mN 373 IARSEHEVSEIIDGLSEQENNEKQMRQLSVIPPMIFDAEQRRVKFINMNG

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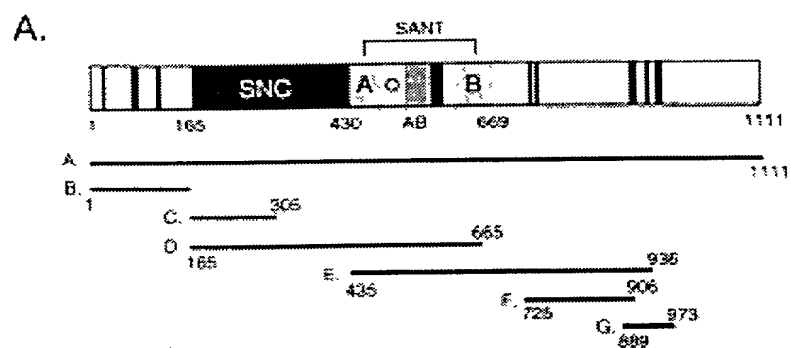
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SANT "B"

Fig. 5



B.

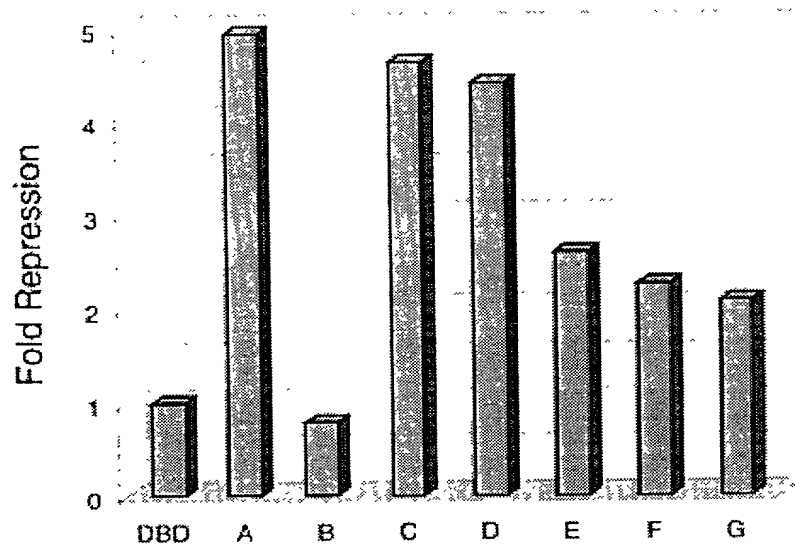


Fig. 6

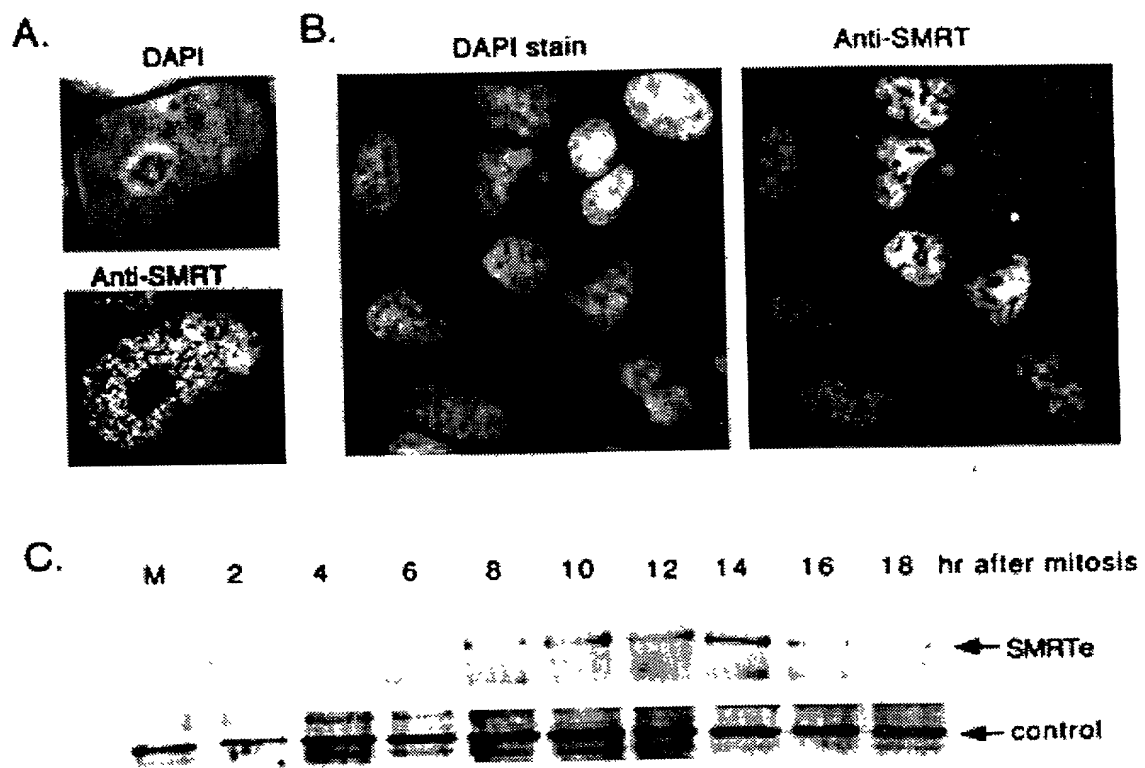


Fig. 7

